

(2)

OIIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/825,144

DATE: 04/20/2001  
TIME: 07:41:14

Input Set : A:\ES.txt  
Output Set: N:\CRF3\04202001\I825144.raw

P.S.

**ENTERED**

3 <110> APPLICANT: Matthias Krause  
4 Antonio S. Sechi  
5 Frank B. Gertler  
6 Jorgen Wehland  
8 <120> TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
10 <130> FILE REFERENCE: M0656/7065  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/825,144  
C--> 12 <141> CURRENT FILING DATE: 2001-04-03  
12 <150> PRIOR APPLICATION NUMBER: US 60/194,215  
13 <151> PRIOR FILING DATE: 2000-04-03  
15 <160> NUMBER OF SEQ ID NOS: 15  
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 15  
21 <212> TYPE: PRT  
22 <213> ORGANISM: Listeria monocytogenes  
24 <400> SEQUENCE: 1  
25 Ser Phe Glu Phe Pro Pro Pro Thr Asp Glu Glu Leu Arg Leu  
26 1 5 10 15  
28 <210> SEQ ID NO: 2  
29 <211> LENGTH: 783  
30 <212> TYPE: PRT  
31 <213> ORGANISM: Homo sapiens  
33 <400> SEQUENCE: 2  
34 Met Ala Lys Tyr Asn Thr Gly Gly Asn Pro Thr Glu Asp Val Ser Val  
35 1 5 10 15  
36 Asn Ser Arg Pro Phe Arg Val Thr Gly Pro Asn Ser Ser Ser Gly Ile  
37 20 25 30  
38 Gln Ala Arg Lys Asn Leu Phe Asn Asn Gln Gly Asn Ala Ser Pro Pro  
39 35 40 45  
40 Ala Gly Pro Ser Asn Val Pro Lys Phe Gly Ser Pro Lys Pro Pro Val  
41 50 55 60  
42 Ala Val Lys Pro Ser Ser Glu Glu Lys Pro Asp Lys Glu Pro Lys Pro  
43 65 70 75 80  
44 Pro Phe Leu Lys Pro Thr Gly Ala Gly Gln Arg Phe Gly Thr Pro Ala  
45 85 90 95  
46 Ser Leu Thr Thr Arg Asp Pro Glu Ala Lys Val Gly Phe Leu Lys Pro  
47 100 105 110  
48 Val Gly Pro Lys Pro Ile Asn Leu Pro Lys Glu Asp Ser Lys Pro Thr  
49 115 120 125  
50 Phe Pro Trp Pro Pro Gly Asn Lys Pro Ser Leu His Ser Val Asn Gln  
51 130 135 140  
52 Asp His Asp Leu Lys Pro Leu Gly Pro Lys Ser Gly Pro Thr Pro Pro  
53 145 150 155 160  
54 Thr Ser Glu Asn Glu Gln Lys Gln Ala Phe Pro Lys Leu Thr Gly Val  
55 165 170 175  
56 Lys Gly Lys Phe Met Ser Ala Ser Gln Asp Leu Glu Pro Lys Pro Leu

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```

57          180          185          190
58 Phe Pro Lys Pro Ala Phe Gly Gln Lys Pro Pro Leu Ser Thr Glu Asn
59          195          200          205
60 Ser His Glu Asp Glu Ser Pro Met Lys Asn Val Ser Ser Ser Lys Gly
61          210          215          220
62 Ser Pro Ala Pro Leu Gly Val Arg Ser Lys Ser Gly Pro Leu Lys Pro
63          225          230          235          240
64 Ala Arg Glu Asp Ser Glu Asn Lys Asp His Ala Gly Glu Ile Ser Ser
65          245          250          255
66 Leu Pro Phe Pro Gly Val Val Leu Lys Pro Ala Ala Ser Arg Gly Gly
67          260          265          270
68 Leu Gly Leu Ser Lys Asn Gly Glu Glu Lys Lys Glu Asp Arg Lys Ile
69          275          280          285
70 Asp Ala Ala Lys Asn Thr Phe Gln Ser Lys Ile Asn Gln Glu Glu Leu
71          290          295          300
72 Ala Ser Gly Thr Pro Pro Ala Arg Phe Pro Lys Ala Pro Ser Lys Leu
73          305          310          315          320
74 Thr Val Gly Gly Pro Trp Gly Gln Ser Gln Glu Lys Glu Lys Gly Asp
75          325          330          335
76 Lys Asn Ser Ala Thr Pro Lys Gln Lys Pro Leu Pro Pro Leu Phe Thr
77          340          345          350
78 Leu Gly Pro Pro Pro Pro Lys Pro Asn Arg Pro Pro Asn Val Asp Leu
79          355          360          365
80 Thr Lys Phe His Lys Thr Ser Ser Gly Asn Ser Thr Ser Lys Gly Gln
81          370          375          380
82 Thr Ser Tyr Ser Thr Thr Ser Leu Pro Pro Pro Pro Pro Ser His Pro
83          385          390          395          400
84 Ala Ser Gln Pro Pro Leu Pro Ala Ser His Pro Ser Gln Pro Pro Val
85          405          410          415
86 Pro Ser Leu Pro Pro Arg Asn Ile Lys Pro Pro Phe Asp Leu Lys Ser
87          420          425          430
88 Pro Val Asn Glu Asp Asn Gln Asp Gly Val Thr His Ser Asp Gly Ala
89          435          440          445
90 Gly Asn Leu Asp Glu Glu Gln Asp Ser Glu Gly Glu Thr Tyr Glu Asp
91          450          455          460
92 Ile Glu Ala Ser Lys Glu Arg Glu Lys Lys Arg Glu Lys Glu Glu Lys
93          465          470          475          480
94 Lys Arg Leu Glu Leu Glu Lys Lys Glu Gln Lys Glu Lys Glu Lys Lys
95          485          490          495
96 Glu Gln Glu Ile Lys Lys Lys Phe Lys Leu Thr Gly Pro Ile Gln Val
97          500          505          510
98 Ile His Leu Ala Lys Ala Cys Cys Asp Val Lys Gly Gly Lys Asn Glu
99          515          520          525
100 Leu Ser Phe Lys Gln Gly Glu Gln Ile Glu Ile Ile Arg Ile Thr Asp
101          530          535          540
102 Asn Pro Glu Gly Lys Trp Leu Gly Arg Thr Ala Arg Gly Ser Tyr Gly
103          545          550          555          560
104 Tyr Ile Lys Thr Thr Ala Val Glu Ile Asp Tyr Asp Ser Leu Lys Leu
105          565          570          575

```

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```

106 Lys Lys Asp Ser Leu Gly Ala Pro Ser Arg Pro Ile Glu Asp Asp Gln
107          580          585          590
108 Glu Val Tyr Asp Asp Val Ala Glu Gln Asp Asp Ile Ser Ser His Ser
109          595          600          605
110 Gln Ser Gly Ser Gly Gly Ile Phe Pro Pro Pro Pro Asp Asp Asp Ile
111          610          615          620
112 Tyr Asp Gly Ile Glu Glu Glu Asp Ala Asp Asp Gly Phe Pro Ala Pro
113          625          630          635          640
114 Pro Lys Gln Leu Asp Met Gly Asp Glu Val Tyr Asp Asp Val Asp Thr
115          645          650          655
116 Ser Asp Phe Pro Val Ser Ser Ala Glu Met Ser Gln Gly Thr Asn Phe
117          660          665          670
118 Gly Lys Ala Lys Thr Glu Glu Lys Asp Leu Lys Lys Leu Lys Lys Gln
119          675          680          685
120 Glu Lys Glu Glu Lys Asp Phe Arg Lys Lys Phe Lys Tyr Asp Gly Glu
121          690          695          700
122 Ile Arg Val Leu Tyr Ser Thr Lys Val Thr Thr Ser Ile Thr Ser Lys
123          705          710          715          720
124 Lys Trp Gly Thr Arg Asp Leu Gln Val Lys Pro Gly Glu Ser Leu Glu
125          725          730          735
126 Val Ile Gln Thr Thr Asp Asp Thr Lys Val Leu Cys Arg Asn Glu Glu
127          740          745          750
128 Gly Lys Tyr Gly Tyr Val Leu Arg Ser Tyr Leu Ala Asp Asn Asp Gly
129          755          760          765
130 Glu Ile Tyr Asp Asp Ile Ala Asp Gly Cys Ile Tyr Asp Asn Asp
131          770          775          780

```

133 &lt;210&gt; SEQ ID NO: 3

134 &lt;211&gt; LENGTH: 2400

135 &lt;212&gt; TYPE: DNA

136 &lt;213&gt; ORGANISM: Homo sapiens

138 &lt;400&gt; SEQUENCE: 3

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139 taggatggaa aggcagatgt aaagtccctc atggcgaaat ataacacggg gggcaacccg      60
140 acagaggatg tctcagtcaa tagccgaccc ttcagagtca cagggccaaa ctcatcttca      120
141 ggaatacaag caagaaagaa cttattcaac aaccaaggaa atgccagccc tcttcgagga      180
142 cccagcaatg tacctaagtt tgggtcccca aagccacctg tggcagtcaa accttcttct      240
143 gaggaagc ctgacaagga acccaagccc ccgtttctaa agcccactgg agcaggccaa      300
144 agattcggaa caccagccag cttgaccacc agagaccccg aggcgaaagt gggatttctg      360
145 aaacctgtag gcccgaagcc catcaacttg cccaaagaag attccaaacc tacatttccc      420
146 tggcctcctg gaaacaagcc atctcttcac agtgtaaacc aagaccatga cttaaagcca      480
147 ctaggcccga aatctgggcc tactcctcca acctcagaaa atgaacagaa gcaagcgttt      540
148 cccaaattga ctggggttaa agggaaattt atgtcagcat cacaagatct tgaacccaag      600
149 cccctcttcc ccaaaccgcg ctttggccag aagccgcccc taagtaccga gaactcccat      660
150 gaagacgaaa gcccctgaa gaatgtgtct tcatcaaaag ggtcccagc tcccctggga      720
151 gtcagggtcca aaagcgcccc tttaaaacca gcaagggaag actcagaaaa taaagaccat      780
152 gcaggggaga tttcaagttt gccctttcct ggagtggttt tgaaacctgc tgcgagcagg      840
153 ggaggcctag gtctctccaa aaatggtgaa gaaaaaagg aagataggaa gatagatgct      900
154 gctaagaaca ccttccagag caaaataaat caggaagagt tggcctcagg gactcctcct      960
155 gccaggttcc ctaaggcccc ttctaagctg acagtggggg ggccatgggg ccaaagtcag      1020
156 gaaaaggaaa agggagacaa gaattcagcc accccgaaac agaagccatt gcctcccttg      1080

```

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```

157 tttaccttgg gtccacctcc accaaaaacc aacagaccac caaatgttga cctgacgaaa 1140
158 ttccacaaaa cctcttctgg aaacagtact agcaaaggcc agacgtctta ctcaacaact 1200
159 tccctgccac caccctccac atcccacccg gccagccaac caccattgcc agcatctcac 1260
160 ccatcacaac caccagtccc aagcctacct ccagaaaaca ttaaaccctcc gtttgacct 1320
161 aaaagccctg tcaatgaaga caatcaagat ggtgtcacgc actctgatgg tgctggaaat 1380
162 ctagatgagg aacaagacag tgaaggagaa acatatgaag acatagaagc atccaaagaa 1440
163 agagagaaga aaagggaaaa ggaagaaaag aagaggttag agctggagaa aaaggaacag 1500
164 aaagagaaag aaaagaaaag acaagaaata aagaagaaat ttaaactaac aggcctatt 1560
165 caagtcatcc atcttgcaaa agcttggtgt gatgtcaaag gaggaagaa tgaactgagc 1620
166 ttcaagcaag gagagcaaat tgaaatcac cgcatacac acaaccaga aggaaaatgg 1680
167 ttgggcagaa gacgaagggg ttcatatggc tatattaaaa caactgctgt agagattgac 1740
168 tatgattctt tgaaactgaa aaaagactct cttggtgccc cttcaagacc tattgaagat 1800
169 gaccaagaag tatatgatga tgttgacag caggatgata ttagcagcca cagtcagagt 1860
170 ggaagtggag ggatattccc tccaccacca gatgatgaca tttatgatgg gattgaagag 1920
171 gaagatgctg atgatggtt cctgtctcct cctaaacaat tggacatggg agatgaagtt 1980
172 tacgatgatg tggatacctc tgatttcctt gtttcacag cagagatgag tcaaggaact 2040
173 aattttggaa aagctaagac agaagaaaag gaccttaaga agctaaaaaa gcaggaaaaa 2100
174 gaagaaaaag acttcaggaa aaaatttaaa tatgatggtg aaattagagt cctatatcca 2160
175 actaaagtta caacttccat aacttctaaa aagtggggaa ccagagatct acaggtaaaa 2220
176 cctggtgaat ctctagaagt tatacaaac acagatgaca caaaagttct ctgcagaaat 2280
177 gaagaaggga aatatggtta tgtccttcgg agttacctag cggacaatga tggagagatc 2340
178 tatgatgata ttgctgatgg ctgcacttat gacaatgact agcactcaac tttggtcatt 2400

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180 <210> SEQ ID NO: 4

181 <211> LENGTH: 829

182 <212> TYPE: PRT

183 <213> ORGANISM: Homo sapiens

185 <400> SEQUENCE: 4

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186 Met Ala Lys Tyr Asn Thr Gly Gly Asn Pro Thr Glu Asp Val Ser Val
187 1 5 10 15
188 Asn Ser Arg Pro Phe Arg Val Thr Gly Pro Asn Ser Ser Ser Gly Ile
189 20 25 30
190 Gln Ala Arg Lys Asn Leu Phe Asn Asn Gln Gly Asn Ala Ser Pro Pro
191 35 40 45
192 Ala Gly Pro Ser Asn Val Pro Lys Phe Gly Ser Pro Lys Pro Pro Val
193 50 55 60
194 Ala Val Lys Pro Ser Ser Glu Glu Lys Pro Asp Lys Glu Pro Lys Pro
195 65 70 75 80
196 Pro Phe Leu Lys Pro Thr Gly Ala Gly Gln Arg Phe Gly Thr Pro Ala
197 85 90 95
198 Ser Leu Thr Thr Arg Asp Pro Glu Ala Lys Val Gly Phe Leu Lys Pro
199 100 105 110
200 Val Gly Pro Lys Pro Ile Asn Leu Pro Lys Glu Asp Ser Lys Pro Thr
201 115 120 125
202 Phe Pro Trp Pro Pro Gly Asn Lys Pro Ser Leu His Ser Val Asn Gln
203 130 135 140
204 Asp His Asp Leu Lys Pro Leu Gly Pro Lys Ser Gly Pro Thr Pro Pro
205 145 150 155 160
206 Thr Ser Glu Asn Glu Gln Lys Gln Ala Phe Pro Lys Leu Thr Gly Val
207 165 170 175

```

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```

208 Lys Gly Lys Phe Met Ser Ala Ser Gln Asp Leu Glu Pro Lys Pro Leu
209           180           185           190
210 Phe Pro Lys Pro Ala Phe Gly Gln Lys Pro Pro Leu Ser Thr Glu Asn
211           195           200           205
212 Ser His Glu Asp Glu Ser Pro Met Lys Asn Val Ser Ser Ser Lys Gly
213           210           215           220
214 Ser Pro Ala Pro Leu Gly Val Arg Ser Lys Ser Gly Pro Leu Lys Pro
215           225           230           235           240
216 Ala Arg Glu Asp Ser Glu Asn Lys Asp His Ala Gly Glu Ile Ser Ser
217           245           250           255
218 Leu Pro Phe Pro Gly Val Val Leu Lys Pro Ala Ala Ser Arg Gly Gly
219           260           265           270
220 Leu Gly Leu Ser Lys Asn Gly Glu Glu Lys Lys Glu Asp Arg Lys Ile
221           275           280           285
222 Asp Ala Ala Lys Asn Thr Phe Gln Ser Lys Ile Asn Gln Glu Glu Leu
223           290           295           300
224 Ala Ser Gly Thr Pro Pro Ala Arg Phe Pro Lys Ala Pro Ser Lys Leu
225           305           310           315           320
226 Thr Val Gly Gly Pro Trp Gly Gln Ser Gln Glu Lys Glu Lys Gly Asp
227           325           330           335
228 Lys Asn Ser Ala Thr Pro Lys Gln Lys Pro Leu Pro Pro Leu Phe Thr
229           340           345           350
230 Leu Gly Pro Pro Pro Pro Lys Pro Asn Arg Pro Pro Asn Val Asp Leu
231           355           360           365
232 Thr Lys Phe His Lys Thr Ser Ser Gly Asn Ser Thr Ser Lys Gly Gln
233           370           375           380
234 Thr Ser Tyr Ser Thr Thr Ser Leu Pro Pro Pro Pro Pro Ser His Pro
235           385           390           395           400
236 Ala Ser Gln Pro Pro Leu Pro Ala Ser His Pro Ser Gln Pro Pro Val
237           405           410           415
238 Pro Ser Leu Pro Pro Arg Asn Ile Lys Pro Pro Phe Asp Leu Lys Ser
239           420           425           430
240 Pro Val Asn Glu Asp Asn Gln Asp Gly Val Thr His Ser Asp Gly Ala
241           435           440           445
242 Gly Asn Leu Asp Glu Glu Gln Asp Ser Glu Gly Glu Thr Tyr Glu Asp
243           450           455           460
244 Ile Glu Ala Ser Lys Glu Arg Glu Lys Lys Arg Glu Lys Glu Glu Lys
245           465           470           475           480
246 Lys Arg Leu Glu Leu Glu Lys Lys Glu Gln Lys Glu Lys Glu Lys Lys
247           485           490           495
248 Glu Gln Glu Ile Lys Lys Lys Phe Lys Leu Thr Gly Pro Ile Gln Val
249           500           505           510
250 Ile His Leu Ala Lys Ala Cys Cys Asp Val Lys Gly Gly Lys Asn Glu
251           515           520           525
252 Leu Ser Phe Lys Gln Gly Glu Gln Ile Glu Ile Ile Arg Ile Thr Asp
253           530           535           540
254 Asn Pro Glu Gly Lys Trp Leu Gly Arg Thr Ala Arg Gly Ser Tyr Gly
255           545           550           555           560
256 Tyr Ile Lys Thr Thr Ala Val Glu Ile Asp Tyr Asp Ser Leu Lys Leu

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/825,144

DATE: 04/20/2001

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Input Set : A:\ES.txt

Output Set: N:\CRF3\04202001\I825144.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8